

>SEQID#1\_SGP037

ATGTCAACAGCTGCCCTTAATTACTTTGGTCAGAAAGTGTTGGGAACCAAGTGAGAGTGCTGCTAAGCTCCCGCCTGCTGCAGGACGACA  
GGCGGTGACACCCACGTGCCACAGCTCCACTTCAGAGCCTAGGTGTTCTCGGTTTGACCCAGATGGTAGTGGAGTCCA GCTACCTGGGACAA  
TTTTGGGATCTGGGATAACCGCATTGATGAGCCAAATCTGCTGCCACCCAGCATTAAGTATGGCAAGCCAAATGCCAAATCAGCTTGGAAAATG  
TGGGTGCGCCTCACAGATTGGCAACCGAAAGAGAAATGAAGATCGGTTTGACTTCGCTCAGCTGACAGATGAGGTCTGTACTTTGCAGTGTA  
TGATGGACACGGTGGACCTGCGACGCA GCTGATTCTGTCTACCCACATGGAGAAATGTAATTATGGATTGCTTCCTAAGGAGAAACTTTGGAA  
ACTCTGTTGACCTTGGCTTTTCTAGAAATAGATAAAGCCTTTTCGAGTCAATGCCCGCTGTCTGCTGATGCAA CTCTTCTGACCTCTGGGACTACT  
GCAACAGTAGCCCTATTGCGAGATGGTATTGAACCTGGTTGTAGCCAGTTTGGGACAGCCGGGCTATTTTGTGTAGAAAGGAAACCCATGA  
AGCTGACCAATTGACCATCTCCAGAAAGAAAGATGAAGAAAGGATCAAGAAATGTGGTGGTTTGTAGCTTGGAAATAGTTTGGGCGAGC  
CTCACGTAAATGGCAGGCTTGCAATGACAAGAAAGTATTGGAGATTGGACCTTAAGACCAAGTGGTGTCTATAGCAAGACCTGAAACTAAGAGGAT  
TAAGTTACATCATGCTGATGACAGCTTCCTGGTCTCACCAAGATGGAATTAACTTCATGGTGAATAGTCAAGAGATTGTGACTTTGTCAATC  
AGTGCCATGATCCCAACGAAGCAGGCCCATGCGGTGACTGAACAGGCAATACAGTACGGTACTGAGGATAACAGTACTGCAGTAGTAGTGCCCTT  
TGGTGCTGGGAAAAATATAAGAACTCTGAAATCAACTTCTCAITTCAGCAGAAAGCTTTGCCTCCAGTGGACGATGGGCGCTGA

>SEQID#2\_SGP037

MSTAALILVRSGGNQRRRLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSPATWDNFGIWDNRIDEPILLPSKYGKPIPKISLENVGCASQIG  
KRKENEDREFDFAQLTDEVLYFAVYDGHGGPAAADFCHTHMEKCMDLLPKEKNLETLTLAFLHDKAFSSHARLSADATLLTSGTTATVALLRDGIEL  
VVASVGDSSRAILCRKGKPMKLTIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRKLHHADDSFLVLTDDGI  
NFMVNSQEICDFVNQCHDPNEAAHAHVTEQAIQYGITEDNSTAVVPFGAWGKYKNSEINFSESFASSGRWA